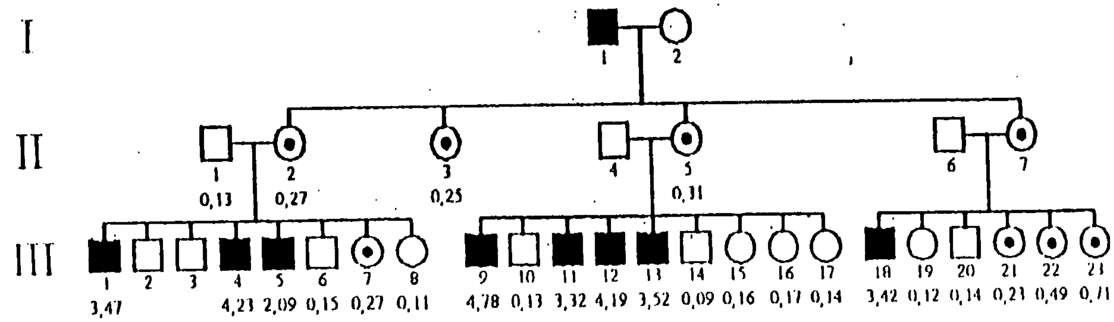


FIG. 1A

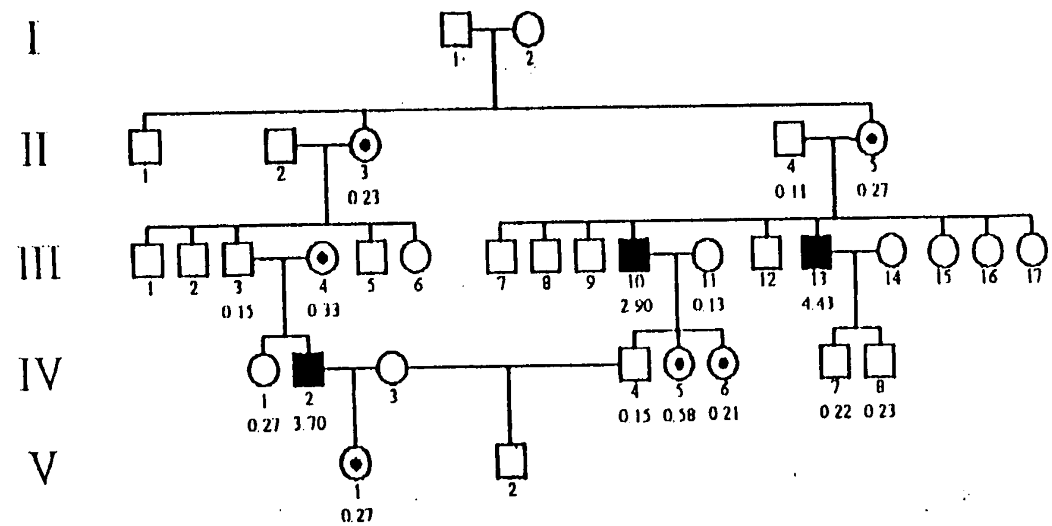


FIG. 1B

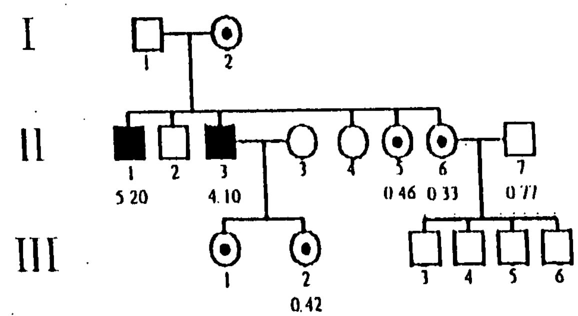


FIG. 1C

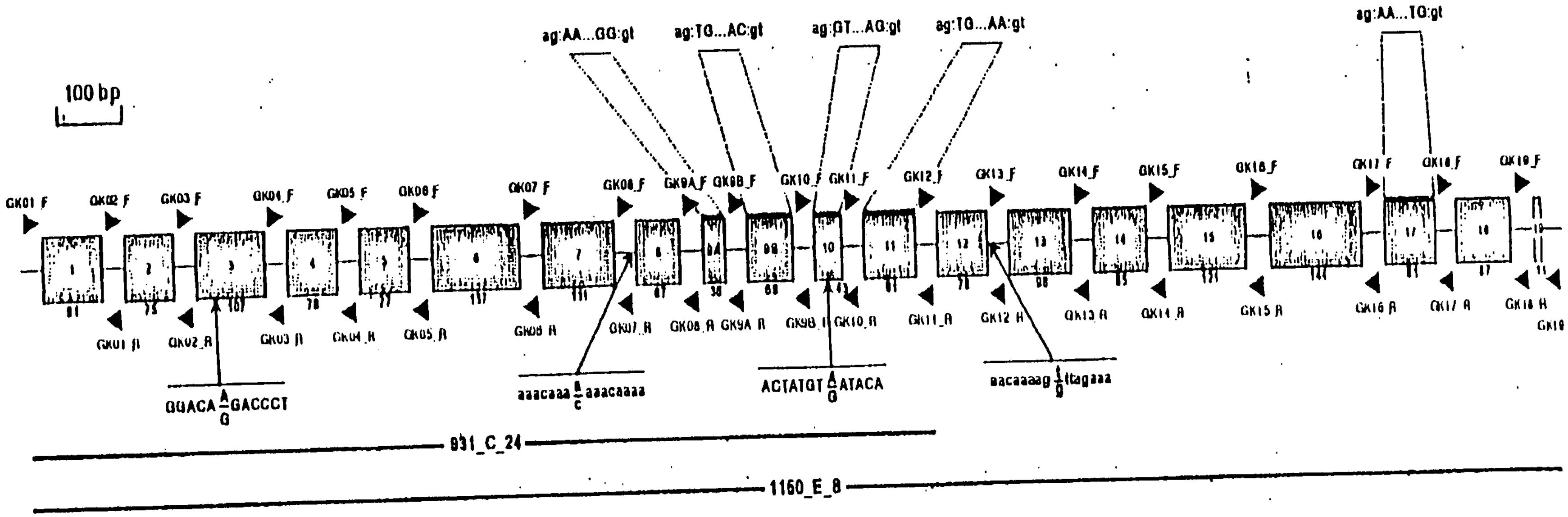
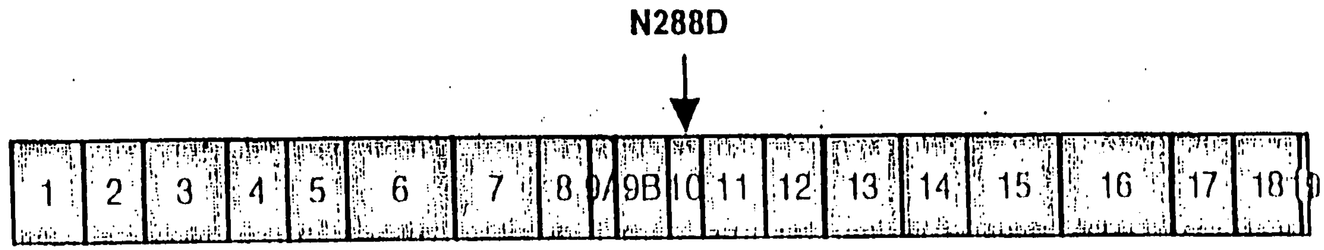

100 bp
ag:AA...GG:gt
ag:TG...AC:gt
ag:GT...AG:gt
ag:TG...AA:gt
ag:AA...TG:gt
GK01_F
GK02_F
GK03_F
GK04_F
GK05_F
GK06_F
GK07_F
GK08_F
GK9A_F
GK9B_F
GK10_F
GK11_F
GK12_F
GK13_F
GK14_F
GK15_F
GK16_F
GK17_F
GK18_F
GK19_F
GK01_R
GK02_R
GK03_R
GK04_R
GK05_R
GK06_R
GK07_R
GK08_R
GK9A_R
GK9B_R
GK10_R
GK11_R
GK12_R
GK13_R
GK14_R
GK15_R
GK16_R
GK17_R
GK18_R
GK19_R
GGACA A/G GACCCT
aaacaaa a/c aaacaaaa
ACTATGT A/G ATACA
aacaaaag t/g ttagaaa
931_C_24
1160_E_8

FIG. 2

FIG. 3A



G TAT GGA ACA GGA TGT TTC TTA CTA TGT $\frac{A}{G}$ AT ACA GGC CAT AAG

FIG. 3B

	270 310	
GK N288D Mutant	FQIGQAKNTYGTGCFLLC**D**TGHKCVFSDHGLLTTVAYKLGR	SEQ ID NO: 6
glpk_human	FQIGQAKNTYGTGCFLLC**N**TGHKCVFSDHGLLTTVAYKLGR	SEQ ID NO: 7
glpk_rat	FQDGQAKNTYGTGCFLLC**N**TGHKCVFSEHGLLTTVAYKLGR	SEQ ID NO: 8
glpk_mouse	FQDGQAKNTYGTGCFLLC**N**TGHKCVFSEHGLLTTVAYKLGR	SEQ ID NO: 9
glpk_ecoli	VKEGMAKNTYGTGCFMLM**N**TGEKAVKSENGLLTTIAC--GP	SEQ ID NO: 10
glpk_pseae	VEPGQAKNTYGTGCFLLM**H**TGDKAVKSTHGLLTTIAC--GP	SEQ ID NO: 11
glpk_entca	FEKGMIKNTYGTGAFIVM**N**TGEEPQLSDNDLLTTIGY--GL	SEQ ID NO: 12
glpk_haein	VHAGQAKNTYGTGCFMLL**H**TGNKAITSKNGLLTTIACNAKG	SEQ ID NO: 13
glpk_bacsu	FEEGMGKNTYGTGCFMLM**N**TGEKAIKSEHGLLTTIAW--GI	SEQ ID NO: 14
glpk_yeast	YKPGAAKCTYGTGCFLLY**N**TGTKKLISQHGALTTLAFWFPH	SEQ ID NO: 15
glpk_mycge	TEPGMVKNTYGTGCFVLM**N**IGDKPTLSKHNLLTTVAWQLEN	SEQ ID NO: 16
glpk_entfa	FEPGMVKNTYGTGSFIVM**N**TGEEPQLSKNNLLTTIGY--GI	SEQ ID NO: 17
glpk_mycpn	VEPAMVKNTYGTGCFMLM**N**IGNELKYSQHNLLTTVAWQLEN	SEQ ID NO: 18
glpk_syny3	DRPGLLKCTYGTGAFLVA**N**TGQTVTRSQHRLLSTVAWTQTN	SEQ ID NO: 19

FIG. 4A

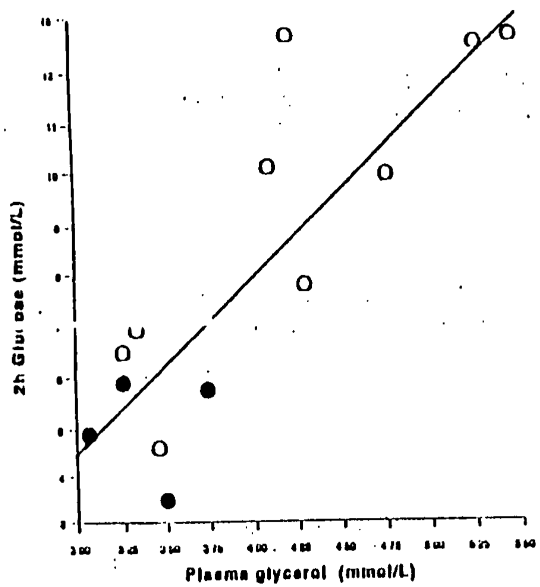


FIG. 4B

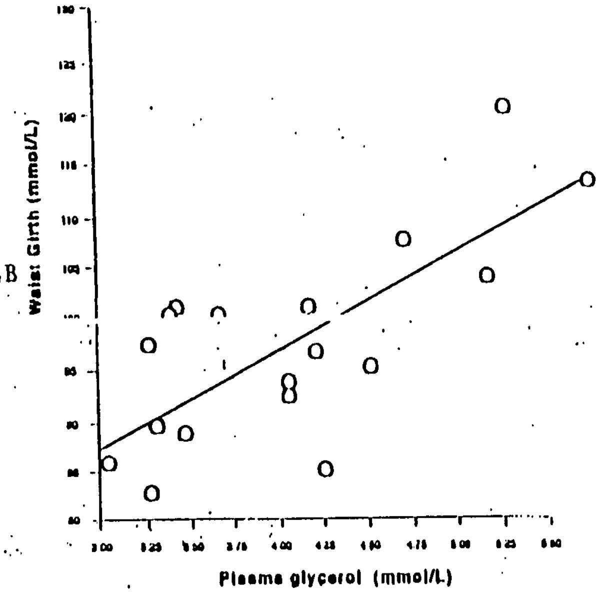


FIG. 4C

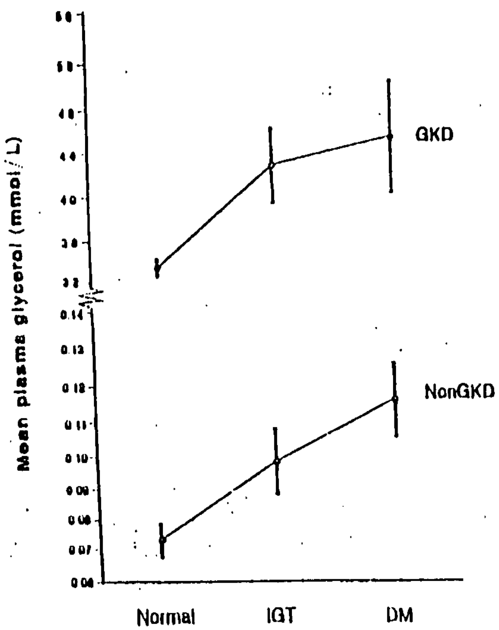
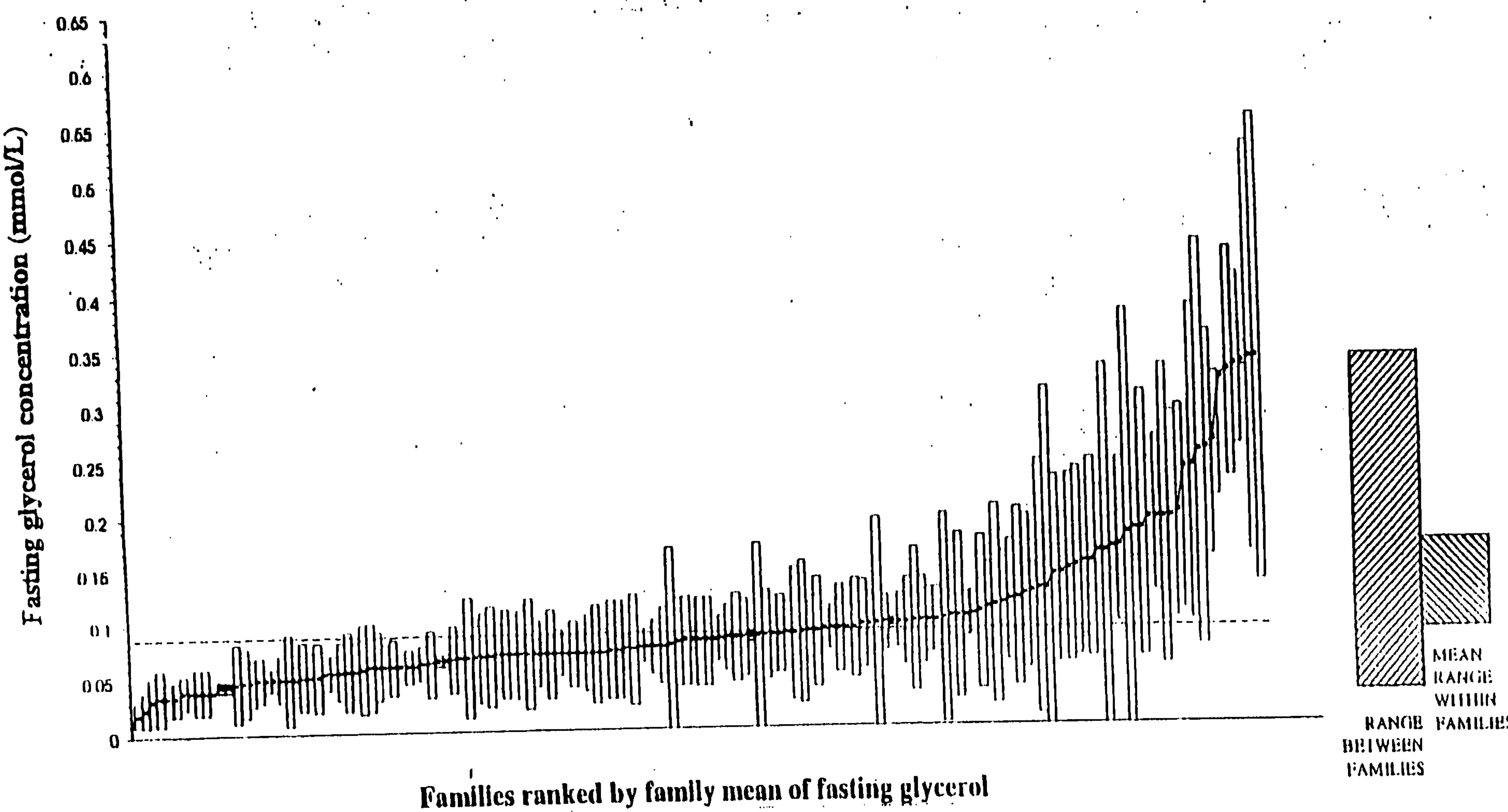


FIG. 5



Fasting glycerol concentration (mmol/L)
0.65
0.6
0.55
0.5
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Families ranked by family mean of fasting glycerol
RANGE BETWEEN FAMILIES
MEAN RANGE WITHIN FAMILIES

poly: A/G
location:13th base of exon 3

ATGCCTTCTTTTGTCAAAGATGGGTGGAACA [A/G] GACCCTAAGGAAATTCTACAT
TCTGTCT SEQ ID NO: 1

CAA vs CAG ==> silent

poly: A/C
location:17th base of intron 8
TAATGGTAAAAAACAAACAAA [A/C] AAACAAAAAACACACCAAAAAACCAA

SEQ ID NO: 2

poly: A/G
location: 29th base of exon 10

TTCATTCTCCCTTCAACCATAGGTATGGAACAGGATGTTTCTTACTATGT [A/G] AT
ACAGGCCATAAGGTtGGTTTTTAATAAAAATGATTAAGTCA SEQ ID NO: 3

AAT vs GAT ==> N to D

poly: G/T
location: 22nd base of intron 12
GAAATTGGTGAGTGTGTTCTAACAAAAG [G/T] TTAGAAAATCTGAAAAATGACACA
TTTCA SEQ ID NO: 4

FIG. 6

SEQ ID NO: 5

Exon 1:
GGTTCAGCGGACGCGCGCGGCCTCGGTCTCTGGACTCGTCACCTGCCCCTCCCCCTCCCGCC
GCCGTCACCCAGGAAACCGGCCGCAATCGCCGGCCGACCTGAAGCTGGTTTCATGGCAGCCT
CAAAGAAGGCAGTTTTGGGGCCATTGGTGGGGGCGGTGGACCAGGGCACCAGTTCGACGCGC
TTTTTGGTGAGCCCGGGGTGACATGTGAAGAGGCGCTGAGC

Exon 2:
TGTAAAACGACGGCCAGTCATCCTTGATATCTGCCTGCATTTTTACATTAATATTACAATAT
CTTTTTCAGGTTTTCAATTCAAAAACAGCTGAACTACTTAGTCATCATCAAGTAGAAATAAA
ACAAGAGTTCCCAAGAGAAGGGTATGTTTCCTAATTTAATATGTAAAGACACATTATGTTTG
TTAGTCCATCTCACCCAACTTGCCC

Exon 3:
CAATGCCTTCTTTTGTCAAAGATGGGTGGAACA [A/G] GACCCTAAGGAAATTCTACATTCT
GTCTATGAGTGTATAGAGAAAACATGTGAGAAACTTGGACAGCTCAATATTGATATTTCCAA
CATAAAAGGTATTTTAGTAGAATATTTTACCCACA

Exon 4:
TGTAAAACGACGGCCAGTTGAGAGCTGTTTTCCTGAAGTAGTTCCTACTTGTTAAATTTTTG
ACTTCCTTCTGTTTAACTTTCTCTTTAAAGCTATTGGTGTCAGCAACCAGAGGGAAACCACT
GTAGTCTGGGACAAGATAACTGGAGAGCCTCTCTACAATGCTGTGGGTAAGCTGTCATGCAT
GGATGTCAAATGTAGGGCCTTTCTTCACATTGCAA

Exon 5:
TGTAAAACGACGGCCAGTTCCTTGATAGTGATTTCAGTAAGTTCTTATTTTTTTAAATGAAG
TTTTTCATGTATATTATTTTATTTTGGTCTATAGTGTGGCTTGATCTAAGAACCCAGTCTAC
CGTTGAGAGTCTTAGTAAAAGAATTCCAGGAAATAATAACTTTGTCAAGGTAAGAATTTCTT
CAGAAGTATACTATAAGAATGTTTCTTTTTTTAAAAAAAGTTTGCAGATTTCACTAGAAAGA
AGCATCTTATGGTACAATAGTTATTTGATACAATTTATAGAATCTTTTTCCCGGATAATTGA
GGCC

Exon 6:
TGTAAAACGACGGCCAGTTTCTTTTGTTTGGTGGTTTTGTTTTAAACTGTTACACTTTTCAT
TTGCTAACTGAACTTCACAACTGCTTTTAGTCCAAGACAGGCCTTCCACTTAGCACTTACTT
CAGTGCAGTGAAACTTCGTTGGCTCCTTGACAATGTGAGAAAAGTTCAAAAGGCCGTTGAAG
AAAAACGAGCTCTTTTTGGGACTATTGATTCATGGCTTATTTGGGTATGTTTAAATATAATG
GATATATGGAGAATTTTTTCAGAAATTTTTTCTAGACTGCCTTGCCTATTGTTTCTACTAGC
AGGTCAGACTTTTTAATTAGCA

FIG. 7A

Exon 7:
TGTAAAACGACGGCCAGTTGTGCTCTGCTGATTATGACCCTTAACAATATGTAAATTAAATT
GCCAATAAGTACAAATTTAACCTGATTTTTTACTCTGCCTAGAGTTTGACAGGAGGAGTCA
ATGGAGGTGTCCACTGTACAGATGTAACAAATGCAAGTAGGACTATGCTTTTCAACATTCAT
TCTTTGGAATGGATAAACAACTCTGCGAGTAAGTTCTGTTTTGCTCTAAATATAGTTTTCC
CAATACACTACCTATTTATAACCGAAATCTTAATATTTTCAGATGTCAGTGGAGCA

Exon 8:
TGTAAAACGACGGCCAGTACAGTGTTAAATACCCAATCTTCTTGTTTTTCAGATTTTTTGGA
ATTCCAATGGAAATTCTTCCAAATGTCCGGAGTTCTTCTGAGATCTATGGCCTAATGGTAAA
AAACAAACAAA [A/C] AAACAAAAAACACACCAAAAAACCAAAAAACAAACAAAAAAAAACC
TAATAATTAAAGTTTTTTTATTACAAAACAAGTTTACTATTCATAATTCAAAAGTCAACTGT
GTTATGTTTTGTGACTTAAAAACTTTACAGTCCTTTTTACAATGG

Exons 9A and 9B
AAAGCTGGGGCCTTGGAAGGTGTGCCAATATCTGGGTAAGTTTCATCACCAAGTGTCTCCC
CATCCCCACCCTTCCCCATGTTATGGCTTTCCTCCTCTTAGTTCATCAGTGTGCCTCTTTTT
AAACTAGGGAAAACAAGTAAAAGTTGCAAAATTGGANNNNTCTTGTTCTTACATGTCATACT
GTGGGCCATTGAGAATCTTTTGAATAAATTAATTTTAACTCTCCCTTCCCATACCTATTATC
TTACATATTAACAAATGGTATTAACAAATGGGGAAAATGGCCAAATGGAGAAAATGCAAGGA
AATAGACAGTTCATTCTTTGATAAATAAAAAATGAAAAATAAATCCTATGGCTCTTCTAAAA
AGAAAGTTAATACTATTGTATTAGTCAGTGTTCTTTATTGTCATTTATACTTTCAGTGTTTA
GGGGACCAGTCTGCTGCATTGGTGGACAAATGTGCTTCCAGATTGGACAAGCCAAAAATAC
GTGAGTTTAAGAAACAGACTTAAAAACCAATGCTGTTTTGTTTTTTCTACTTGGTGCTTTGA
ATAAGGAAAAGCTTTTGAAGTTCATCCAGGATGAAAATCAATAGCTTAATAGCTCCAATATG
CATATATACACTTTTTACCATTTTTTTATATCTTTAAATAAAATACAAAA
TGCCATATATATGCACACTGATGAAGCTTATAAAGACCTAAATTTGTAGGCTGGGCGCGG

Exons 10 and 11:
TTATTTGCTTTCAATAAAATTGTCTTCTATTCATTCTCCCTTCAACCATAGGTATGGAACAG
GATGTTTCTTACTATGT [A/G] ATACAGGCCATAAGGTTGGTTTTTTAAATTAAAAAATTGA
TTTAAAAGTCTAAGTTCATCTAAATAATGCTTGAACATAATTTACTATTAAACAACTTTTAG
TCTTTAGCTTTTACTTAATCTTTATCAGGGTTTAATTTAGAGCTCAATACAAAATTTGAATC
GTTCTAATAAGAACCATTTTAGACTCTTTGAATTTTATATGTGTGTTTTTAATTGTGCTGGG
GGGAAATCTAGACTGAGACCTCATCAAATTCTTAATGCAAATCTAATTTGAAACAAGGAATA
AACTTTTTATACAGCTTAAATGTGTTCTTAATTCTGATCGTTTTGACTGTAAGGATTTATTT
TAAAAATTGGTTTATTGATTGCATTATTTTGTACCTATGTTATTTTAACTTTAAAAAAAAGT
TCTCATGTTATCTTTTCATTTTCCACTACTGAAATCTTTTTTTTTTCTTTCTTACAGTGTGT
ATTTTCTGATCATGGCCTTCTCACCACAGTGGCTTACAAACTTGGCAGAGACAAACCAGTAT
ATTATGCTTTGGAAGTAAGTTCTTTTTAATCAATATGGATAATATGACAAACATTCAAAGCT
AATAAAAATCACAGAGTTTTCTAACACTTTTCTGGTAAATCTTAATACAGAGGACTCAAAAA
GTTCTGCTTTCTTGGCATTTGATTGAGTTGAAGGAACCTGAAACTGATCTGGGTGTCAGGAC
TCACAGGAGACCTTGATTAGATTGGTTCCTCAGTTCTTATGCCAATTAATCATGTCACCTTA
GGCATATTACTTGAGAGCTCTACAATGTGAGGTTTTTTTTTTTTTTTATCTCTAAAGTTTAAT
CGGATTAACGTGCTCTCTAACATTTCTTTCATCTTGAAAATTCTTTGATTTTATAAATAAAA
TGCTCCAGTGTTCCAAAGAGAACCCTGGGCACAAATAGGCAGAACAACTCTCTTCACTTGTC
TCCTCATAAAAATAAATTTTGTGTAACATTTTGATATAGAAAAGAAAGCGACGAGATTTATG
CCACTTATCACTGGAAACATTTGTTTCAACATTTTTGTATGTTATAGTAGGAATATGCCAG
CCTAAGCCTATA

FIG. 7B

Exon 12:
TTTTATTAGTGACTTAGATAAAACTATGTTTGTATTAGAAGACCTAGTTTACATATTTGTCG
GAGTCTCAAAATGGAAACTGAATTCTGTCCATCTGATTGTGTCATACACAGAATATGCTCAA
TAAAAACCTTGGATAGTGATAAAATATATTCTGTCTTGAATTCCTTTTTTTCTTTAGGGTTC
TGTAGCTATAGCTGGTGCTGTTATTCGCTGGCTAAGAGACAATCTTGGAATTATAAAGACCT
CAGAAGAAATTGGTGAGTGTGTTCTAACAAAAG [G/T] TTAGAAAATCTGAAAAATGACACA
TTTCAGTATTTTATCTCTGCAAAGTAAATATCGATGCTTTGCCCCAAATGTGAT

Exon 13:
CCAGTTGTGTGATTTTTGTTTTGTTTTGTTTTAATGTTAGAAAAACTTGCTAAAGAAGTAGG
TACTTCTTATGGCTGCTACTTCGTCCCAGCATTTTCGGGGTAATATGCACCTTATTGGAGC
CCAGCGCAAGAGGGTAAGTATTGAAAATATGGAGTGCTTTTGGGGATCTTGATTTAT

Exons 14 and 15:
TGTAAAACGACGGCCAGTTGATTATGTCCAATTTTCTCTTCCTGGACATTTCTGTCTACCAA
ATTTGACCTTTTCATATTTGAGATATTTCAAATTGATTGGTTTATATCATTCTAATCTGAAA
ATCTTTGTGCGTATTTTTAGGATAATCTGTGGACTCACTCAGTTCACCAATAAATGCCATAT
TGCTTTTGCTGCATTAGAAGCTGTTTGTTTCCAAACTCGAGAGGTAACAAATATGGCCTGT
TTTCTTGTACTTAGTTCACTTTTATCACTCTTAAGTTATATGTTAACACCCGAGATTTATTC
AGTACTGAAAATGTAGTTAATCAAATATTAAGGCTGCCTAAATACTAATCTAAATATAAGCA
GGGTTTTCCCCCTTTTTCCAGCTGTCATTACCTTCTAAGTTCCTGTTCCCTGTCAGGCACTG
GGAAATTTATGGTTGTGGGAGGCTGAGTGGCACACATTAGGCAAAGGAAACAGCACAAACA
TAGGCATCaAGGCAGAAAAACAGGGTGCAAAATAGAGTTGTATAGCTTAGCTGAATATCAAG
GTGAATGCAGAGGTGTAGTGAGAGAAAAGGTTGGCTGTGACCAGATCAAAGAGGGCTTAGAA
GACCAGAATAAGAAGTCTCAATTTATTCCATAGGCTCTTGGAAGCTCTTGAGAGTTTCTGAG
TGGAGGATTGCCATTTTCAGAGATGTTACTATGAAATAGATTTATAACATTAATTGCACTGG
TTTATTTAAGATTTTGGATGCCATGAATCGAGACTGTGGAATTCCACTCAGTCATTTGCAGG
TAGATGGAGGAATGACCAGCAACAAAATTCTTATGCAGCTACAAGCAGACATTCTGTATATA
CCAGTAGGTTAGTAAGTCTTCATTCCTTTAAACTCCCAGAGTAATGTTTCTTGTGGAATAAC
TAGTTCTTTGGG

Exon 16:
TGTAAAACGACGGCCAGTTCCCAGAGTAATGTTTCTTGTGGAATAACTAGTTCTTTGGGCAT
ATGTAACCACAAAGATATTGATGGAACTCTCTCTCCTCAGTGAAGCCCTCAATGCCCGAAAC
CACTGCACTGGGTGCGGCTATGGCGGCAGGGGCTGCAGAAGGAGTCGGCGTATGGAGTCTCG
AACCCGAGGATTTGTCTGCCGTCACGATGGAGCGGTTTGAACCTCAGATTAATGCGGAGGGT
ACATTTAAAGAATGAAATGTTCAGTGATATACTGTGAAAACGACCTTAGTGCACGGGAGTTT
TGTTTTTCTGTTTAGTTAAAAGTTAAGGAACCAAGTAAAATAGTAAATGTTATCATTGCAGA
TTCGGCTGCCAAGCATATTGGGCTTTACTGAATAAATGTGAATGAGAGAAATCGTTGCTTAT
CAAAAGAACTTCTAAAATCACTTTTTAAAAATCATT

Exon 17:
TGTAAAACGACGGCCAGTAGCCCTACTGCAGTTTAATGTGTCAATAATTTGTCAAGAATGTT
GAGTGATCATAAGTATGGTACTAAGAACATCTCAGCAAACTACCTTTCGTTATGTGTTTTTT
CTACCTTCTAATTCTAGAAAGTGAAATTCGTTATTCTACATGGAAGAAAGCTGTGATGAAGT
CAATGGGTTGGGTTACAACTCAATCTCCAGAAAGTGGTAAAAATGTTTTTGTTTATTATTGT
CACATTTTCTTAGTATATTAAATAGTTATTTAAGTATCTAGGCATTTACACATAGCCAGGCT
GCTCTGAAGAAAAGCATTATCATATGTCCAGAGATTCTGACATTTTGAAAACACTTTAAAGT
TCTAAACACAAAATGTAAATTATCAGGTGT

FIG. 7C

Exon 18:
TGTAAAACGACGGCCAGTTGGTTTGGTTTGCTTGACTGGAATCTCTTCTGCTTGGATGACCA
CAGGTGACCCTAGTATCTTCTGTAGTCTGCCCTTGGGCTTTTTTATAGTGAGTAGCATGGTA
ATGTTAATCGGAGCAAGGTACATCTCAGGTTAGTTACTCTTTAAATTAGACAACTCTATTAG
TTAGCTTTAATGTTTTCGTGTATAACTTAGCAGAAATTTTTCAGTGTTTTTCATTCTTTCTG
TGTCTAGGAAGCTGGAAAATCAATTAAAGGTCTAATTAGTTAGACCAATTAATCTTTGGGGG
CAGTTAGAAGTAAGAACTGTGACTCTGCTTACCCTTTTTAAATTTTTAATGTGATGACTTCT
TTAAGAGGGACTACATTCTGCTGTCAGCTGCAGCAATAAGCAAAAGTGAAAATACTAATATT
TAAATGACAGGACTTTCAGACTGACTGCTGAAAGTTAAAGTATACTT

Exon 19:
AAAATTACTGGCTTAAATGGAAATGATGCTTCTTATTCTGTATGTTCCCATGAAAGTGAAAC
TTAAAAAAAAAATTCATGATTAGGGTTTCATGAAAAGGCCTTGTTTCTATGAAAATTGAGAC
AGGTTGCATCTCTCTAAGCTAAAAGATGGGCTATGTGTCTAGAGTCTTAGACTTCTAAAATG
CATGTGGTCACTATATGTAGGTTATCTCTTCGGTGACATACACTGCAATTTGAGAGGGCTGG
AAATTGTTTGCCTTGGTAAACGATTAGCAACAGTGGCAATATTTGTTAATTTTGGAATTGGC
CCTGTTTGTTGCATTTTAATTGTGAGGCATGATTTAGAAATCATATGGACTTTCTAGCTTAA
TAAATGATTGAATCATCTGCATTGCTTTAACTCCTGAATTGTATGCATGTATTATTGACATA
TATGGTTTTTGTTCCCCATTTCAGGTATTCCATAAAACCTACCAACTCATGGATTCCCAAGA
TGTGAGCTTTTTACATAATGAAAGAACCCAGCAATTCTGTCTCTTAATGCAATGACACTATT
CATAGACTTTGATTTTATTTATAAGCCACTTGCTGCATGACCCTCCAAGTAGACCTGTGGCT
TAAAATAAAGAAAATGCAGCAAAAAGAATGCTATAGAAATATTTGGTGGTTTTTTTTTTTTT
TAAACATCCACAGTTAAGGTTGGGCCAGCTACCTTTGGGGCTGACCCCCTCCATTGCCATAA
CATCCTGCTCCATTCCCTCTAAGATGTAGGAAGAATTCGGATCCTTACCATTGGAATCTTCC
ATCGAACATACTCAAACACTTTTGGACCAGGATTTGAGTCTCTGCATGACATATACTTGATT
AAAAGGTTATTACTAACCTGTTAAAAATCAGCAGCTCTTTGCTTTTAAGAGACACCCTAAAA
GTCTTCTTTTCTACATAGTTGAAGACAGCAACATCTTCACTGAATGTTTGAATAGAAACCTC
TACTAAATTATTAAAATAGACATTTAGTGTTCTCACAGCTTGGATATTTTTCTGAAAAGTTA
TTTGCCAAAACTGAAATCCTTCAGATGTTTTCCATGGTCCCACTAATTATAATGACTTTCTG
TCTGGGTCTTATAGGAAAAGATACTTTCTTTTTTCTTCCATCTTTCCTTTTTATATTTTTTA
CTTTGTATGTATAACATACATGCCTATATATTTTATACACTGAGGGAGCCCATTTATAAATA
AAGAGCACATTATATTCAGAAGGTTCTAACAGGG

FIG. 7D

TABLE 1

Characteristics of carriers of the N288D GK gene mutation and of their unaffected relatives

	Men			Women		
	N288D carriers	Unaffected relatives	p	N288D carriers	Unaffected relatives	p
N	18	18		14	14	
Age (years)	46,4±14,2	42,0±18,8	0.32	44,9±13,5	43,7±17,8	0.87
Uncorrected triglyceride (mmol/L)[(1)]	6,26±1,13	2,05±0,54	<0,0001	2,84±1,20	1,30±0,65	0.0002
Glycerol (mmol/L)	3,99±0,71	0,10±0,04	<0,0001	0,54±0,14	0,10±0,02	<0,0001
Corrected triglyceride (mmol/L)[(1)]	2,27±0,75	1,95±0,53	<0,0001	2,31±1,22	1,19±0,67	0.03
Free fatty acid (mmol/L)	0,77±0,22	0,57±0,25	0.01	1,29±0,35	0,76±0,17	0.0004
Fasting glucose (mmol/L)	5,2±0,74	4,8±0,31	0.13	5,0±0,7	4,6±0,3	0.10
2h glucose following OGTT (mmol/L)	7,9±3,1	5,8±1,6	0.02	7,0±6,1	5,0±2,1	0.04
Fasting insulin (mU/L)[(1)]	13,3±14,0	15,1±14,8	0.62	12,2±13,1	9,0±3,4	0.60
Waist girth (cm)	97,7±9,3	88,1±12,3	0.01	88,5±3,8	79,3±5,8	0.03
Body mass index (kg/m^2)	27,9±4,1	24,9±3,9	0.03	28,1±5,5	23,1±2,3	0.001
% total body fat	27,1±7,2	22,9±7,6	0.01	46,3±3,1	33,9±11,3	0.001

(1) geometric mean, p value after log transformation

Figure 8

TABLE 2

Fasting plasma glycerol concentration (mmol/L) in the initial cohort of 1056 individuals, by risk factor of glucose intolerance and diabetes mellitus

			No.	Glycerol geometric mean ± SD	p
Gender	men		717	0.065 ± 0.081	<0.0001
	women	- premenopaused	137	0.071 ± 0.093	
		- menopaused	202	0.099 ± 0.085	
Age (Y)		<50	486	0.071 ± 0.082	
		50 - 60	408	0.076 ± 0.106	0.0015
		>60	165	0.083 ± 0.053	
Fasting glucose (mmol/L)		< 5.2	449	0.068 ± 0.080	
		5.2 - 5.9	336	0.070 ± 0.090	<0.0001
		6.0 - 6.9	271	0.090 ± 0.100	
Fasting insulin (UI)		<15	637	0.067 ± 0.082	0.02
		≥15	419	0.086 ± 0.101	
2 hours glucose (mmol/L)		<7.8	572	0.062 ± 0.071	
		7.8 - 11.0	283	0.081 ± 0.101	<0.0001
		≥11.1	201	0.102 ± 0.110	
Triglyceride (mmol/L)		≤ 2.2	389	0.057 ± 0.062	<0.0001
		>2.2	667	0.082 ± 0.103	
Free fatty acid (mmol/L)		< 0.6	589	0.066 ± 0.054	<0.0001
		≥0.6	467	0.111 ± 0.112	
Body mass index (kg/m2)		≤ 27	428	0.060 ± 0.087	<0.0001
		>27	628	0.079 ± 0.097	

p value from one-way ANOVA

Figure 9

TABLE 3. Multivariate analysis of the relationships of fasting pla[illegible]ma glycerol concentration with impaired glucose toleranc[illegible] (2h glucose 7,8-11,0 mmol/L following a 75 g oral lo[illegible]d) before and after adjustment for covariates identified i[illegible]

	Model 1	Model 2	Model 3	Mod[illegible]l 4
Glycerol (log)				
ß	1.75	1.62	1.46	0.7[illegible]
Odds ratio	5.76	5.42	4.33	2.4[illegible]
p	<0,0001	<0,0001	<0,0001	0.0[illegible]
Triglyceride (log)				
ß		0.54	0.35	0.1[illegible]
Odds ratio		1.75	1.42	1.1[illegible]
p		0.02	0.11	0.6[illegible]
Body mass index (kg/m²)				
ß			0.10	0.0[illegible]
Odds ratio			1.10	1.0[illegible]
p			<0.0001	0.0[illegible]
Fasting insulin (log)				
ß				0.[illegible]7
Odds ratio				1.[illegible]
p				0.[illegible]9
Fasting glucose (mmol/L)				
ß				1.1[illegible]
Odds ratio				2.[illegible]5
p				<0,0[illegible]01
Free fatty acid (log)				
ß				1.[illegible]2
Odds ratio				4.[illegible]3
p				0.0[illegible]7

Odds ratios are expressed as the increase in the risk of 2h glucose •7,3 m[illegible]mol/L following a 75 g oral charge, associated with a 1-SD increase in the va[illegible]iables studied. ß denotes the standardized estimate which is the parameter estim[illegible]te of each variable in the multivariate logistic model. All models included [illegible] and gender as covariates. Otherwise, only the variables included in each mo[illegible]el are shown. Subjects with severe hyperglycemlemia due to the N788D mutation i[illegible] the

Figure 10